

S1 Text. Supplementary References

91. Chandramohan R, Wu PY, Phan JH, Wang MD. Benchmarking RNA-Seq quantification tools. Conference proceedings : Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual Conference. 2013;2013:647-50. Epub 2013/10/11. doi: 10.1109/EMBC.2013.6609583. PubMed PMID: 24109770.
92. Steijger T, Abril JF, Engstrom PG, Kokocinski F, Hubbard TJ, Guigo R, et al. Assessment of transcript reconstruction methods for RNA-seq. *Nature methods*. 2013;10(12):1177-84. Epub 2013/11/05. doi: 10.1038/nmeth.2714. PubMed PMID: 24185837; PubMed Central PMCID: PMC3851240.
93. George NI, Chang CW. DAFS: a data-adaptive flag method for RNA-sequencing data to differentiate genes with low and high expression. *BMC bioinformatics*. 2014;15:92. Epub 2014/04/02. doi: 10.1186/1471-2105-15-92. PubMed PMID: 24685233; PubMed Central PMCID: PMC4098771.
94. Angelini C, De Canditiis D, De Feis I. Computational approaches for isoform detection and estimation: good and bad news. *BMC bioinformatics*. 2014;15:135. Epub 2014/06/03. doi: 10.1186/1471-2105-15-135. PubMed PMID: 24885830; PubMed Central PMCID: PMC4098781.
95. Dillies MA, Rau A, Aubert J, Hennequet-Antier C, Jeanmougin M, Servant N, et al. A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. *Briefings in bioinformatics*. 2013;14(6):671-83. Epub 2012/09/19. doi: 10.1093/bib/bbs046. PubMed PMID: 22988256.
96. Pabinger S, Dander A, Fischer M, Snajder R, Sperk M, Efremova M, et al. A survey of tools for variant analysis of next-generation genome sequencing data. *Briefings in bioinformatics*. 2014;15(2):256-78. Epub 2013/01/24. doi: 10.1093/bib/bbs086. PubMed PMID: 23341494; PubMed Central PMCID: PMC3956068.
97. Castle JC, Loewer M, Boegel S, Tadmor AD, Boisguerin V, de Graaf J, et al. Mutated tumor alleles are expressed according to their DNA frequency. *Scientific reports*. 2014;4:4743. Epub 2014/04/23. doi: 10.1038/srep04743. PubMed PMID: 24752137; PubMed Central PMCID: PMC3994436.
98. Wang Q, Xia J, Jia P, Pao W, Zhao Z. Application of next generation sequencing to human gene fusion detection: computational tools, features and perspectives. *Briefings in bioinformatics*. 2013;14(4):506-19. Epub 2012/08/11. doi: 10.1093/bib/bbs044. PubMed PMID: 22877769; PubMed Central PMCID: PMC3713712.
99. Mertens F, Tayebwa J. Evolving techniques for gene fusion detection in soft tissue tumours. *Histopathology*. 2014;64(1):151-62. Epub 2013/12/11. doi: 10.1111/his.12272. PubMed PMID: 24320890.
100. Kreuze JF, Perez A, Untiveros M, Quispe D, Fuentes S, Barker I, et al. Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: a generic method for diagnosis, discovery and sequencing of viruses. *Virology*. 2009;388(1):1-7. Epub 2009/04/28. doi: 10.1016/j.virol.2009.03.024. PubMed PMID: 19394993.
101. Tang KW, Alaei-Mahabadi B, Samuelsson T, Lindh M, Larsson E. The landscape of viral expression and host gene fusion and adaptation in human cancer. *Nature communications*. 2013;4:2513. Epub 2013/10/03. doi: 10.1038/ncomms3513. PubMed PMID: 24085110; PubMed Central PMCID: PMC3806554.
102. Hooper JE. A survey of software for genome-wide discovery of differential splicing in RNA-Seq data. *Human genomics*. 2014;8:3. Epub 2014/01/23. doi: 10.1186/1479-7364-8-3. PubMed PMID: 24447644; PubMed Central PMCID: PMC3903050.

103. Li X, Nair A, Wang S, Wang L. Quality Control of RNA-Seq Experiments. *Methods in molecular biology*. 2015;1269:137-46. Epub 2015/01/13. doi: 10.1007/978-1-4939-2291-8_8. PubMed PMID: 25577376.
104. Yang X, Liu D, Liu F, Wu J, Zou J, Xiao X, et al. HTQC: a fast quality control toolkit for Illumina sequencing data. *BMC bioinformatics*. 2013;14:33. Epub 2013/02/01. doi: 10.1186/1471-2105-14-33. PubMed PMID: 23363224; PubMed Central PMCID: PMC3571943.
105. Guo Y, Zhao S, Sheng Q, Ye F, Li J, Lehmann B, et al. Multi-perspective quality control of Illumina exome sequencing data using QC3. *Genomics*. 2014;103(5-6):323-8. Epub 2014/04/08. doi: 10.1016/j.ygeno.2014.03.006. PubMed PMID: 24703969.
106. Anvar SY, Khachatryan L, Vermaat M, van Galen M, Pulyakhina I, Ariyurek Y, et al. Determining the quality and complexity of next-generation sequencing data without a reference genome. *Genome biology*. 2014;15(12):555. Epub 2014/12/18. doi: 10.1186/s13059-014-0555-3. PubMed PMID: 25514851; PubMed Central PMCID: PMC4298064.
107. Del Fabbro C, Scalabrin S, Morgante M, Giorgi FM. An extensive evaluation of read trimming effects on Illumina NGS data analysis. *PloS one*. 2013;8(12):e85024. Epub 2014/01/01. doi: 10.1371/journal.pone.0085024. PubMed PMID: 24376861; PubMed Central PMCID: PMC3871669.
108. Dodt M, Roehr JT, Ahmed R, Dieterich C. FLEXBAR-Flexible Barcode and Adapter Processing for Next-Generation Sequencing Platforms. *Biology (Basel)*. 2012;1(3):895-905. doi: 10.3390/biology1030895. PubMed PMID: 24832523; PubMed Central PMCID: PMC4009805.
109. Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome biology*. 2013;14(4):R36. Epub 2013/04/27. doi: 10.1186/gb-2013-14-4-r36. PubMed PMID: 23618408; PubMed Central PMCID: PMC4053844.
110. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. *Bioinformatics*. 2013;29(1):15-21. Epub 2012/10/30. doi: 10.1093/bioinformatics/bts635. PubMed PMID: 23104886; PubMed Central PMCID: PMC3530905.
111. Kim D, Langmead B, Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. *Nature methods*. 2015;12(4):357-60. doi: 10.1038/nmeth.3317. PubMed PMID: 25751142.
112. Hoffmann S, Otto C, Doose G, Tanzer A, Langenberger D, Christ S, et al. A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. *Genome biology*. 2014;15(2):R34. doi: 10.1186/gb-2014-15-2-r34. PubMed PMID: 24512684; PubMed Central PMCID: PMC4056463.
113. Wang K, Singh D, Zeng Z, Coleman SJ, Huang Y, Savich GL, et al. MapSplice: accurate mapping of RNA-seq reads for splice junction discovery. *Nucleic acids research*. 2010;38(18):e178. Epub 2010/08/31. doi: 10.1093/nar/gkq622. PubMed PMID: 20802226; PubMed Central PMCID: PMC2952873.
114. Butterfield YS, Kreitzman M, Thiessen N, Corbett RD, Li Y, Pang J, et al. JAGuar: junction alignments to genome for RNA-seq reads. *PloS one*. 2014;9(7):e102398. doi: 10.1371/journal.pone.0102398. PubMed PMID: 25062255; PubMed Central PMCID: PMC4111418.
115. Au KF, Jiang H, Lin L, Xing Y, Wong WH. Detection of splice junctions from paired-end RNA-seq data by SpliceMap. *Nucleic acids research*. 2010;38(14):4570-8. doi: 10.1093/nar/gkq211. PubMed PMID: 20371516; PubMed Central PMCID: PMC2919714.
116. Dimon MT, Sorber K, DeRisi JL. HMMSplicer: a tool for efficient and sensitive discovery of known and novel splice junctions in RNA-Seq data. *PloS one*. 2010;5(11):e13875. doi:

- 10.1371/journal.pone.0013875. PubMed PMID: 21079731; PubMed Central PMCID: PMC2975632.
117. Burns PD, Li Y, Ma J, Borodovsky M. UnSplicer: mapping spliced RNA-Seq reads in compact genomes and filtering noisy splicing. *Nucleic acids research*. 2014;42(4):e25. doi: 10.1093/nar/gkt1141. PubMed PMID: 24259430; PubMed Central PMCID: PMC3936741.
118. Fonseca NA, Rung J, Brazma A, Marioni JC. Tools for mapping high-throughput sequencing data. *Bioinformatics*. 2012;28(24):3169-77. Epub 2012/10/13. doi: 10.1093/bioinformatics/bts605. PubMed PMID: 23060614.
119. Hatem A, Bozdag D, Toland AE, Catalyurek UV. Benchmarking short sequence mapping tools. *BMC bioinformatics*. 2013;14:184. Epub 2013/06/14. doi: 10.1186/1471-2105-14-184. PubMed PMID: 23758764; PubMed Central PMCID: PMC3694458.
120. Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome biology*. 2009;10(3):R25. doi: 10.1186/gb-2009-10-3-r25. PubMed PMID: 19261174; PubMed Central PMCID: PMC2690996.
121. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics*. 2009;25(14):1754-60. doi: 10.1093/bioinformatics/btp324. PubMed PMID: 19451168; PubMed Central PMCID: PMC2705234.
122. Kroll KW, Mokaram NE, Pelletier AR, Frankhouser DE, Westphal MS, Stump PA, et al. Quality Control for RNA-Seq (QuaCRS): An Integrated Quality Control Pipeline. *Cancer informatics*. 2014;13(Suppl 3):7-14. doi: 10.4137/CIN.S14022. PubMed PMID: 25368506; PubMed Central PMCID: PMC4214596.
123. Wang L, Wang S, Li W. RSeQC: quality control of RNA-seq experiments. *Bioinformatics*. 2012;28(16):2184-5. doi: 10.1093/bioinformatics/bts356. PubMed PMID: 22743226.
124. DeLuca DS, Levin JZ, Sivachenko A, Fennell T, Nazaire MD, Williams C, et al. RNA-SeQC: RNA-seq metrics for quality control and process optimization. *Bioinformatics*. 2012;28(11):1530-2. doi: 10.1093/bioinformatics/bts196. PubMed PMID: 22539670; PubMed Central PMCID: PMC3356847.
125. Lassmann T, Hayashizaki Y, Daub CO. SAMStat: monitoring biases in next generation sequencing data. *Bioinformatics*. 2011;27(1):130-1. doi: 10.1093/bioinformatics/btq614. PubMed PMID: 21088025; PubMed Central PMCID: PMC3008642.
126. Cabanski CR, Wilkerson MD, Soloway M, Parker JS, Liu J, Prins JF, et al. BlackOPs: increasing confidence in variant detection through mappability filtering. *Nucleic acids research*. 2013;41(19):e178. doi: 10.1093/nar/gkt692. PubMed PMID: 23935067; PubMed Central PMCID: PMC3799449.
127. Jones DC, Ruzzo WL, Peng X, Katze MG. A new approach to bias correction in RNA-Seq. *Bioinformatics*. 2012;28(7):921-8. doi: 10.1093/bioinformatics/bts055. PubMed PMID: 22285831; PubMed Central PMCID: PMC3315719.
128. Schurch NJ, Cole C, Sherstnev A, Song J, Duc C, Storey KG, et al. Improved annotation of 3' untranslated regions and complex loci by combination of strand-specific direct RNA sequencing, RNA-Seq and ESTs. *PloS one*. 2014;9(4):e94270. Epub 2014/04/12. doi: 10.1371/journal.pone.0094270. PubMed PMID: 24722185; PubMed Central PMCID: PMC3983147.
129. Ortogero N, Hennig GW, Luong D, Yan W. Computer-assisted annotation of small RNA transcriptomes. *Methods in molecular biology*. 2015;1218:353-64. Epub 2014/10/17. doi: 10.1007/978-1-4939-1538-5_22. PubMed PMID: 25319663.
130. Musacchia F, Basu S, Petrosino G, Salvemini M, Sanges R. Annocript: a flexible pipeline for the annotation of transcriptomes able to identify putative long noncoding RNAs. *Bioinformatics*. 2015. doi: 10.1093/bioinformatics/btv106. PubMed PMID: 25701574.

131. Zhu Y, Li M, Sousa AM, Sestan N. XSAAnno: a framework for building ortholog models in cross-species transcriptome comparisons. *BMC genomics*. 2014;15:343. doi: 10.1186/1471-2164-15-343. PubMed PMID: 24884593; PubMed Central PMCID: PMC4035071.
132. Lomsadze A, Burns PD, Borodovsky M. Integration of mapped RNA-Seq reads into automatic training of eukaryotic gene finding algorithm. *Nucleic acids research*. 2014;42(15):e119. doi: 10.1093/nar/gku557. PubMed PMID: 24990371; PubMed Central PMCID: PMC4150757.
133. Sharma P, Mantri SS. WImpiBLAST: web interface for mpiBLAST to help biologists perform large-scale annotation using high performance computing. *PloS one*. 2014;9(6):e101144. doi: 10.1371/journal.pone.0101144. PubMed PMID: 24979410; PubMed Central PMCID: PMC4076281.
134. Bischler T, Kopf M, Voss B. Transcript mapping based on dRNA-seq data. *BMC bioinformatics*. 2014;15:122. doi: 10.1186/1471-2105-15-122. PubMed PMID: 24780064; PubMed Central PMCID: PMC4016656.
135. Amman F, Wolfinger MT, Lorenz R, Hofacker IL, Stadler PF, Findeiss S. TSSAR: TSS annotation regime for dRNA-seq data. *BMC bioinformatics*. 2014;15:89. doi: 10.1186/1471-2105-15-89. PubMed PMID: 24674136; PubMed Central PMCID: PMC4098767.
136. Lu Z, Matera AG. Vicinal: a method for the determination of ncRNA ends using chimeric reads from RNA-seq experiments. *Nucleic acids research*. 2014;42(9):e79. doi: 10.1093/nar/gku207. PubMed PMID: 24623808; PubMed Central PMCID: PMC4027162.
137. Liu J, Xiao H, Huang S, Li F. OMIGA: Optimized Maker-Based Insect Genome Annotation. *Mol Genet Genomics*. 2014;289(4):567-73. doi: 10.1007/s00438-014-0831-7. PubMed PMID: 24609470.
138. Ryvkin P, Leung YY, Ungar LH, Gregory BD, Wang LS. Using machine learning and high-throughput RNA sequencing to classify the precursors of small non-coding RNAs. *Methods*. 2014;67(1):28-35. doi: 10.1016/j.ymeth.2013.10.002. PubMed PMID: 24145223; PubMed Central PMCID: PMC3991776.
139. Jones M, Blaxter M. afterParty: turning raw transcriptomes into permanent resources. *BMC bioinformatics*. 2013;14:301. doi: 10.1186/1471-2105-14-301. PubMed PMID: 24093729; PubMed Central PMCID: PMC3856601.
140. Axtell MJ. ShortStack: comprehensive annotation and quantification of small RNA genes. *Rna*. 2013;19(6):740-51. doi: 10.1261/rna.035279.112. PubMed PMID: 23610128; PubMed Central PMCID: PMC3683909.
141. Gao Y, Wang J, Zhao F. CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. *Genome biology*. 2015;16(1):4. doi: 10.1186/s13059-014-0571-3. PubMed PMID: 25583365; PubMed Central PMCID: PMC4316645.
142. Gomes CP, Cho JH, Hood L, Franco OL, Pereira RW, Wang K. A Review of Computational Tools in microRNA Discovery. *Frontiers in genetics*. 2013;4:81. Epub 2013/05/31. doi: 10.3389/fgene.2013.00081. PubMed PMID: 23720668; PubMed Central PMCID: PMC3654206.
143. Zhang Z, Jiang L, Wang J, Gu P, Chen M. MTide: an integrated tool for the identification of miRNA-target interaction in plants. *Bioinformatics*. 2015;31(2):290-1. doi: 10.1093/bioinformatics/btu633. PubMed PMID: 25256573.
144. Hoogstrate Y, Jenster G, Martens-Uzunova ES. FlaiMapper: computational annotation of small ncRNA-derived fragments using RNA-seq high-throughput data. *Bioinformatics*. 2015;31(5):665-73. doi: 10.1093/bioinformatics/btu696. PubMed PMID: 25338717.
145. An J, Lai J, Sajjanhar A, Lehman ML, Nelson CC. miRPlant: an integrated tool for identification of plant miRNA from RNA sequencing data. *BMC bioinformatics*. 2014;15:275.

doi: 10.1186/1471-2105-15-275. PubMed PMID: 25117656; PubMed Central PMCID: PMC4141084.

146. Marsico A, Huska MR, Lasserre J, Hu H, Vucicevic D, Musahl A, et al. PROmiRNA: a new miRNA promoter recognition method uncovers the complex regulation of intronic miRNAs. *Genome biology*. 2013;14(8):R84. doi: 10.1186/gb-2013-14-8-r84. PubMed PMID: 23958307; PubMed Central PMCID: PMC4053815.

147. Muller S, Rycak L, Winter P, Kahl G, Koch I, Rotter B. omiRas: a Web server for differential expression analysis of miRNAs derived from small RNA-Seq data. *Bioinformatics*. 2013;29(20):2651-2. doi: 10.1093/bioinformatics/btt457. PubMed PMID: 23946503.

148. Alon S, Erew M, Eisenberg E. DREAM: a webserver for the identification of editing sites in mature miRNAs using deep sequencing data. *Bioinformatics*. 2015. doi: 10.1093/bioinformatics/btv187. PubMed PMID: 25840043.

149. Lu B, Zeng Z, Shi T. Comparative study of de novo assembly and genome-guided assembly strategies for transcriptome reconstruction based on RNA-Seq. *Science China Life sciences*. 2013;56(2):143-55. Epub 2013/02/09. doi: 10.1007/s11427-013-4442-z. PubMed PMID: 23393030.

150. Guttman M, Garber M, Levin JZ, Donaghey J, Robinson J, Adiconis X, et al. Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. *Nature biotechnology*. 2010;28(5):503-10. doi: 10.1038/nbt.1633. PubMed PMID: 20436462; PubMed Central PMCID: PMC2868100.

151. Perteau M, Perteau GM, Antonescu CM, Chang TC, Mendell JT, Salzberg SL. StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. *Nature biotechnology*. 2015;33(3):290-5. doi: 10.1038/nbt.3122. PubMed PMID: 25690850.

152. Maretty L, Sibbesen JA, Krogh A. Bayesian transcriptome assembly. *Genome biology*. 2014;15(10):501. doi: 10.1186/s13059-014-0501-4. PubMed PMID: 25367074; PubMed Central PMCID: PMC4397945.

153. Li W, Feng J, Jiang T. IsoLasso: a LASSO regression approach to RNA-Seq based transcriptome assembly. *J Comput Biol*. 2011;18(11):1693-707. doi: 10.1089/cmb.2011.0171. PubMed PMID: 21951053; PubMed Central PMCID: PMC3216102.

154. Schliesky S, Gowik U, Weber AP, Brautigam A. RNA-Seq Assembly - Are We There Yet? *Frontiers in plant science*. 2012;3:220. Epub 2012/10/12. doi: 10.3389/fpls.2012.00220. PubMed PMID: 23056003; PubMed Central PMCID: PMC3457010.

155. Misner I, Bicep C, Lopez P, Halary S, Baptiste E, Lane CE. Sequence comparative analysis using networks: software for evaluating de novo transcript assembly from next-generation sequencing. *Molecular biology and evolution*. 2013;30(8):1975-86. Epub 2013/05/15. doi: 10.1093/molbev/mst087. PubMed PMID: 23666209; PubMed Central PMCID: PMC3708500.

156. Amin S, Prentis PJ, Gilding EK, Pavasovic A. Assembly and annotation of a non-model gastropod (*Nerita melanotragus*) transcriptome: a comparison of de novo assemblers. *BMC research notes*. 2014;7:488. Epub 2014/08/03. doi: 10.1186/1756-0500-7-488. PubMed PMID: 25084827; PubMed Central PMCID: PMC4124492.

157. Finseth FR, Harrison RG. A comparison of next generation sequencing technologies for transcriptome assembly and utility for RNA-Seq in a non-model bird. *PloS one*. 2014;9(10):e108550. Epub 2014/10/04. doi: 10.1371/journal.pone.0108550. PubMed PMID: 25279728; PubMed Central PMCID: PMC4184788.

158. Janes J, Hu F, Lewin A, Turro E. A comparative study of RNA-seq analysis strategies. *Briefings in bioinformatics*. 2015. Epub 2015/03/20. doi: 10.1093/bib/bbv007. PubMed PMID: 25788326.

159. Haas BJ, Papanicolaou A, Yassour M, Grabherr M, Blood PD, Bowden J, et al. De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nature protocols*. 2013;8(8):1494-512. doi: 10.1038/nprot.2013.084. PubMed PMID: 23845962; PubMed Central PMCID: PMC3875132.
160. Schulz MH, Zerbino DR, Vingron M, Birney E. Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. *Bioinformatics*. 2012;28(8):1086-92. doi: 10.1093/bioinformatics/bts094. PubMed PMID: 22368243; PubMed Central PMCID: PMC3324515.
161. Li B, Dewey CN. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC bioinformatics*. 2011;12:323. doi: 10.1186/1471-2105-12-323. PubMed PMID: 21816040; PubMed Central PMCID: PMC3163565.
162. Le HS, Schulz MH, McCauley BM, Hinman VF, Bar-Joseph Z. Probabilistic error correction for RNA sequencing. *Nucleic acids research*. 2013;41(10):e109. doi: 10.1093/nar/gkt215. PubMed PMID: 23558750; PubMed Central PMCID: PMC3664804.
163. Bao E, Jiang T, Girke T. BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. *Bioinformatics*. 2013;29(10):1250-9. doi: 10.1093/bioinformatics/btt127. PubMed PMID: 23493323.
164. Chu HT, Hsiao WW, Chen JC, Yeh TJ, Tsai MH, Lin H, et al. EBARDenovo: highly accurate de novo assembly of RNA-Seq with efficient chimera-detection. *Bioinformatics*. 2013;29(8):1004-10. doi: 10.1093/bioinformatics/btt092. PubMed PMID: 23457040.
165. Chang Z, Li G, Liu J, Zhang Y, Ashby C, Liu D, et al. Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. *Genome biology*. 2015;16:30. doi: 10.1186/s13059-015-0596-2. PubMed PMID: 25723335; PubMed Central PMCID: PMC4342890.
166. Roberts A, Pachter L. Streaming fragment assignment for real-time analysis of sequencing experiments. *Nature methods*. 2013;10(1):71-3. doi: 10.1038/nmeth.2251. PubMed PMID: 23160280; PubMed Central PMCID: PMC3880119.
167. Patro R, Mount SM, Kingsford C. Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. *Nature biotechnology*. 2014;32(5):462-4. doi: 10.1038/nbt.2862. PubMed PMID: 24752080; PubMed Central PMCID: PMC4077321.
168. Zhang Z, Wang W. RNA-Skim: a rapid method for RNA-Seq quantification at transcript level. *Bioinformatics*. 2014;30(12):i283-i92. doi: 10.1093/bioinformatics/btu288. PubMed PMID: 24931995; PubMed Central PMCID: PMC4058932.
169. Behr J, Kahles A, Zhong Y, Sreedharan VT, Drewe P, Ratsch G. MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. *Bioinformatics*. 2013;29(20):2529-38. doi: 10.1093/bioinformatics/btt442. PubMed PMID: 23980025; PubMed Central PMCID: PMC3789545.
170. Mezlini AM, Smith EJ, Fiume M, Buske O, Savich GL, Shah S, et al. iReckon: simultaneous isoform discovery and abundance estimation from RNA-seq data. *Genome research*. 2013;23(3):519-29. doi: 10.1101/gr.142232.112. PubMed PMID: 23204306; PubMed Central PMCID: PMC3589540.
171. Mangul S, Caciula A, Glebova O, Mandoiu I, Zelikovsky A. Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. *In Silico Biol*. 2011;11(5-6):251-61. doi: 10.3233/ISB-2012-0459. PubMed PMID: 23202426.
172. Anders S, Pyl PT, Huber W. HTSeq—a Python framework to work with high-throughput sequencing data. *Bioinformatics*. 2015;31(2):166-9. Epub 2014/09/28. doi: 10.1093/bioinformatics/btu638. PubMed PMID: 25260700; PubMed Central PMCID: PMC4287950.

173. Liao Y, Smyth GK, Shi W. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. *Bioinformatics*. 2014;30(7):923-30. doi: 10.1093/bioinformatics/btt656. PubMed PMID: 24227677.
174. Schmid MW, Grossniklaus U. Rcount: simple and flexible RNA-Seq read counting. *Bioinformatics*. 2015;31(3):436-7. doi: 10.1093/bioinformatics/btu680. PubMed PMID: 25322836.
175. Finotello F, Lavezzo E, Bianco L, Barzon L, Mazzon P, Fontana P, et al. Reducing bias in RNA sequencing data: a novel approach to compute counts. *BMC bioinformatics*. 2014;15 Suppl 1:S7. doi: 10.1186/1471-2105-15-S1-S7. PubMed PMID: 24564404; PubMed Central PMCID: PMC4016203.
176. Hashimoto TB, Edwards MD, Gifford DK. Universal count correction for high-throughput sequencing. *PLoS computational biology*. 2014;10(3):e1003494. doi: 10.1371/journal.pcbi.1003494. PubMed PMID: 24603409; PubMed Central PMCID: PMC3945112.
177. Sharma CM, Vogel J. Differential RNA-seq: the approach behind and the biological insight gained. *Current opinion in microbiology*. 2014;19:97-105. Epub 2014/07/16. doi: 10.1016/j.mib.2014.06.010. PubMed PMID: 25024085.
178. Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, et al. limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic acids research*. 2015;43(7):e47. doi: 10.1093/nar/gkv007. PubMed PMID: 25605792.
179. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology*. 2014;15(12):550. doi: 10.1186/s13059-014-0550-8. PubMed PMID: 25516281; PubMed Central PMCID: PMC4302049.
180. Robinson MD, McCarthy DJ, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*. 2010;26(1):139-40. doi: 10.1093/bioinformatics/btp616. PubMed PMID: 19910308; PubMed Central PMCID: PMC2796818.
181. Davidson NM, Oshlack A. Corset: enabling differential gene expression analysis for de novo assembled transcriptomes. *Genome biology*. 2014;15(7):410. doi: 10.1186/s13059-014-0410-6. PubMed PMID: 25063469; PubMed Central PMCID: PMC4165373.
182. Yu D, Huber W, Vitek O. Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size. *Bioinformatics*. 2013;29(10):1275-82. doi: 10.1093/bioinformatics/btt143. PubMed PMID: 23589650; PubMed Central PMCID: PMC3654711.
183. Gu J, Wang X, Halakivi-Clarke L, Clarke R, Xuan J. BADGE: a novel Bayesian model for accurate abundance quantification and differential analysis of RNA-Seq data. *BMC bioinformatics*. 2014;15 Suppl 9:S6. doi: 10.1186/1471-2105-15-S9-S6. PubMed PMID: 25252852; PubMed Central PMCID: PMC4168709.
184. Sonesson C. compcodeR--an R package for benchmarking differential expression methods for RNA-seq data. *Bioinformatics*. 2014;30(17):2517-8. doi: 10.1093/bioinformatics/btu324. PubMed PMID: 24813215.
185. Rau A, Marot G, Jaffrezic F. Differential meta-analysis of RNA-seq data from multiple studies. *BMC bioinformatics*. 2014;15:91. doi: 10.1186/1471-2105-15-91. PubMed PMID: 24678608; PubMed Central PMCID: PMC4021464.
186. Clark NR, Hu KS, Feldmann AS, Kou Y, Chen EY, Duan Q, et al. The characteristic direction: a geometrical approach to identify differentially expressed genes. *BMC bioinformatics*. 2014;15:79. doi: 10.1186/1471-2105-15-79. PubMed PMID: 24650281; PubMed Central PMCID: PMC4000056.

187. Bi Y, Davuluri RV. NPEBseq: nonparametric empirical bayesian-based procedure for differential expression analysis of RNA-seq data. *BMC bioinformatics*. 2013;14:262. doi: 10.1186/1471-2105-14-262. PubMed PMID: 23981227; PubMed Central PMCID: PMC3765716.
188. Chen L. *Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing*. *Statistics in biosciences*. 2013;5(1):138-55. Epub 2013/09/24. doi: 10.1007/s12561-012-9064-7. PubMed PMID: 24058384; PubMed Central PMCID: PMC3776476.
189. Alamancos GP, Agirre E, Eyraas E. Methods to study splicing from high-throughput RNA sequencing data. *Methods in molecular biology*. 2014;1126:357-97. Epub 2014/02/20. doi: 10.1007/978-1-62703-980-2_26. PubMed PMID: 24549677.
190. Li HD, Menon R, Omenn GS, Guan Y. The emerging era of genomic data integration for analyzing splice isoform function. *Trends in genetics : TIG*. 2014;30(8):340-7. Epub 2014/06/22. doi: 10.1016/j.tig.2014.05.005. PubMed PMID: 24951248; PubMed Central PMCID: PMC4112133.
191. Liu R, Loraine AE, Dickerson JA. Comparisons of computational methods for differential alternative splicing detection using RNA-seq in plant systems. *BMC bioinformatics*. 2014;15(1):364. Epub 2014/12/17. doi: 10.1186/s12859-014-0364-4. PubMed PMID: 25511303; PubMed Central PMCID: PMC4271460.
192. Anders S, Reyes A, Huber W. Detecting differential usage of exons from RNA-seq data. *Genome research*. 2012;22(10):2008-17. doi: 10.1101/gr.133744.111. PubMed PMID: 22722343; PubMed Central PMCID: PMC3460195.
193. Niu L, Huang W, Umbach DM, Li L. IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. *BMC genomics*. 2014;15:862. doi: 10.1186/1471-2164-15-862. PubMed PMID: 25283306; PubMed Central PMCID: PMC4195885.
194. Gatto A, Torroja-Fungairino C, Mazzarotto F, Cook SA, Barton PJ, Sanchez-Cabo F, et al. FineSplice, enhanced splice junction detection and quantification: a novel pipeline based on the assessment of diverse RNA-Seq alignment solutions. *Nucleic acids research*. 2014;42(8):e71. doi: 10.1093/nar/gku166. PubMed PMID: 24574529; PubMed Central PMCID: PMC4005686.
195. Hu Y, Liu Y, Mao X, Jia C, Ferguson JF, Xue C, et al. PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. *Nucleic acids research*. 2014;42(3):e20. doi: 10.1093/nar/gkt1304. PubMed PMID: 24362841; PubMed Central PMCID: PMC3919567.
196. Bernard E, Jacob L, Mairal J, Vert JP. Efficient RNA isoform identification and quantification from RNA-Seq data with network flows. *Bioinformatics*. 2014;30(17):2447-55. doi: 10.1093/bioinformatics/btu317. PubMed PMID: 24813214; PubMed Central PMCID: PMC4147886.
197. Mudvari P, Movassagh M, Kowsari K, Seyfi A, Kokkinaki M, Edwards NJ, et al. SNPllice: variants that modulate Intron retention from RNA-sequencing data. *Bioinformatics*. 2015;31(8):1191-8. doi: 10.1093/bioinformatics/btu804. PubMed PMID: 25481010; PubMed Central PMCID: PMC4393518.
198. Vitting-Seerup K, Porse BT, Sandelin A, Waage J. spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC bioinformatics*. 2014;15:81. doi: 10.1186/1471-2105-15-81. PubMed PMID: 24655717; PubMed Central PMCID: PMC3998036.
199. Park JW, Tokheim C, Shen S, Xing Y. Identifying differential alternative splicing events from RNA sequencing data using RNASEq-MATS. *Methods in molecular biology*. 2013;1038:171-9. doi: 10.1007/978-1-62703-514-9_10. PubMed PMID: 23872975.

200. Aschoff M, Hotz-Wagenblatt A, Glatting KH, Fischer M, Eils R, König R. SplicingCompass: differential splicing detection using RNA-seq data. *Bioinformatics*. 2013;29(9):1141-8. doi: 10.1093/bioinformatics/btt101. PubMed PMID: 23449093.
201. Hu Y, Huang Y, Du Y, Orellana CF, Singh D, Johnson AR, et al. DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. *Nucleic acids research*. 2013;41(2):e39. doi: 10.1093/nar/gks1026. PubMed PMID: 23155066; PubMed Central PMCID: PMC3553996.
202. Kimes PK, Cabanski CR, Wilkerson MD, Zhao N, Johnson AR, Perou CM, et al. SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. *Nucleic acids research*. 2014;42(14):e113. doi: 10.1093/nar/gku521. PubMed PMID: 25030904; PubMed Central PMCID: PMC4132703.
203. Pulyakhina I, Gazzoli I, t Hoen PA, Verwey N, Dunnen JD, Aartsma-Rus A, et al. SplicePie: a novel analytical approach for the detection of alternative, non-sequential and recursive splicing. *Nucleic acids research*. 2015. doi: 10.1093/nar/gkv242. PubMed PMID: 25800735.
204. Jia C, Hu Y, Liu Y, Li M. Mapping Splicing Quantitative Trait Loci in RNA-Seq. *Cancer informatics*. 2015;14(Suppl 1):45-53. Epub 2015/03/04. doi: 10.4137/CIN.S24832. PubMed PMID: 25733796; PubMed Central PMCID: PMC4333812.
205. McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, et al. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome research*. 2010;20(9):1297-303. doi: 10.1101/gr.107524.110. PubMed PMID: 20644199; PubMed Central PMCID: PMC2928508.
206. Goya R, Sun MG, Morin RD, Leung G, Ha G, Wiegand KC, et al. SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. *Bioinformatics*. 2010;26(6):730-6. doi: 10.1093/bioinformatics/btq040. PubMed PMID: 20130035; PubMed Central PMCID: PMC2832826.
207. Tang X, Baheti S, Shameer K, Thompson KJ, Wills Q, Niu N, et al. The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. *Nucleic acids research*. 2014;42(22):e172. doi: 10.1093/nar/gku1005. PubMed PMID: 25352556; PubMed Central PMCID: PMC4267611.
208. Wang C, Davila JI, Baheti S, Bhagwate AV, Wang X, Kocher JP, et al. RVboost: RNA-seq variants prioritization using a boosting method. *Bioinformatics*. 2014;30(23):3414-6. doi: 10.1093/bioinformatics/btu577. PubMed PMID: 25170027; PubMed Central PMCID: PMC4296157.
209. Monlong J, Calvo M, Ferreira PG, Guigo R. Identification of genetic variants associated with alternative splicing using sQTLseeker. *Nature communications*. 2014;5:4698. doi: 10.1038/ncomms5698. PubMed PMID: 25140736; PubMed Central PMCID: PMC4143934.
210. Peralta M, Combes MC, Cenci A, Lashermes P, Dereeper A. SNIploid: A Utility to Exploit High-Throughput SNP Data Derived from RNA-Seq in Allopolyploid Species. *Int J Plant Genomics*. 2013;2013:890123. doi: 10.1155/2013/890123. PubMed PMID: 24163691; PubMed Central PMCID: PMC3791807.
211. Nijveen H, van Kaauwen M, Esselink DG, Hoegen B, Vosman B. QualitySNPng: a user-friendly SNP detection and visualization tool. *Nucleic acids research*. 2013;41(Web Server issue):W587-90. doi: 10.1093/nar/gkt333. PubMed PMID: 23632165; PubMed Central PMCID: PMC3692117.
212. Miller AC, Obholzer ND, Shah AN, Megason SG, Moens CB. RNA-seq-based mapping and candidate identification of mutations from forward genetic screens. *Genome research*. 2013;23(4):679-86. doi: 10.1101/gr.147322.112. PubMed PMID: 23299976; PubMed Central PMCID: PMC3613584.

213. Philippe N, Salson M, Commes T, Rivals E. CRAC: an integrated approach to the analysis of RNA-seq reads. *Genome biology*. 2013;14(3):R30. doi: 10.1186/gb-2013-14-3-r30. PubMed PMID: 23537109; PubMed Central PMCID: PMC4053775.
214. Radenbaugh AJ, Ma S, Ewing A, Stuart JM, Collisson EA, Zhu J, et al. RADIA: RNA and DNA integrated analysis for somatic mutation detection. *PLoS one*. 2014;9(11):e111516. doi: 10.1371/journal.pone.0111516. PubMed PMID: 25405470; PubMed Central PMCID: PMC4236012.
215. Ramaswami G, Zhang R, Piskol R, Keegan LP, Deng P, O'Connell MA, et al. Identifying RNA editing sites using RNA sequencing data alone. *Nature methods*. 2013;10(2):128-32. Epub 2013/01/08. doi: 10.1038/nmeth.2330. PubMed PMID: 23291724; PubMed Central PMCID: PMC3676881.
216. Lee JH, Ang JK, Xiao X. Analysis and design of RNA sequencing experiments for identifying RNA editing and other single-nucleotide variants. *Rna*. 2013;19(6):725-32. Epub 2013/04/20. doi: 10.1261/rna.037903.112. PubMed PMID: 23598527; PubMed Central PMCID: PMC3683905.
217. Nigita G, Veneziano D, Ferro A. A-to-I RNA Editing: Current Knowledge Sources and Computational Approaches with Special Emphasis on Non-Coding RNA Molecules. *Frontiers in bioengineering and biotechnology*. 2015;3:37. Epub 2015/04/11. doi: 10.3389/fbioe.2015.00037. PubMed PMID: 25859542; PubMed Central PMCID: PMC4373398.
218. Picardi E, Pesole G. REDIttools: high-throughput RNA editing detection made easy. *Bioinformatics*. 2013;29(14):1813-4. doi: 10.1093/bioinformatics/btt287. PubMed PMID: 23742983.
219. Zhang Q, Xiao X. Genome sequence-independent identification of RNA editing sites. *Nature methods*. 2015;12(4):347-50. doi: 10.1038/nmeth.3314. PubMed PMID: 25730491; PubMed Central PMCID: PMC4382388.
220. Suzuki T, Ueda H, Okada S, Sakurai M. Transcriptome-wide identification of adenosine-to-inosine editing using the ICE-seq method. *Nature protocols*. 2015;10(5):715-32. doi: 10.1038/nprot.2015.037. PubMed PMID: 25855956.
221. Stevenson KR, Coolon JD, Wittkopp PJ. Sources of bias in measures of allele-specific expression derived from RNA-sequence data aligned to a single reference genome. *BMC genomics*. 2013;14:536. Epub 2013/08/08. doi: 10.1186/1471-2164-14-536. PubMed PMID: 23919664; PubMed Central PMCID: PMC3751238.
222. Liu Z, Yang J, Xu H, Li C, Wang Z, Li Y, et al. Comparing computational methods for identification of allele-specific expression based on next generation sequencing data. *Genetic epidemiology*. 2014;38(7):591-8. Epub 2014/09/04. doi: 10.1002/gepi.21846. PubMed PMID: 25183311.
223. Leon-Novelo LG, McIntyre LM, Fear JM, Graze RM. A flexible Bayesian method for detecting allelic imbalance in RNA-seq data. *BMC genomics*. 2014;15:920. Epub 2014/10/24. doi: 10.1186/1471-2164-15-920. PubMed PMID: 25339465; PubMed Central PMCID: PMC4230747.
224. Pandey RV, Franssen SU, Futschik A, Schlotterer C. Allelic imbalance metre (Allim), a new tool for measuring allele-specific gene expression with RNA-seq data. *Mol Ecol Resour*. 2013;13(4):740-5. doi: 10.1111/1755-0998.12110. PubMed PMID: 23615333; PubMed Central PMCID: PMC3739924.
225. Pirinen M, Lappalainen T, Zaitlen NA, Consortium GT, Dermitzakis ET, Donnelly P, et al. Assessing allele-specific expression across multiple tissues from RNA-seq read data. *Bioinformatics*. 2015. doi: 10.1093/bioinformatics/btv074. PubMed PMID: 25819081.
226. Mayba O, Gilbert HN, Liu J, Haverty PM, Jhunjhunwala S, Jiang Z, et al. MBASED: allele-specific expression detection in cancer tissues and cell lines. *Genome biology*.

2014;15(8):405. doi: 10.1186/s13059-014-0405-3. PubMed PMID: 25315065; PubMed Central PMCID: PMC4165366.

227. Chen Y, Yao H, Thompson EJ, Tannir NM, Weinstein JN, Su X. VirusSeq: software to identify viruses and their integration sites using next-generation sequencing of human cancer tissue. *Bioinformatics*. 2013;29(2):266-7. doi: 10.1093/bioinformatics/bts665. PubMed PMID: 23162058; PubMed Central PMCID: PMC3546792.

228. Wang Q, Jia P, Zhao Z. VirusFinder: software for efficient and accurate detection of viruses and their integration sites in host genomes through next generation sequencing data. *PloS one*. 2013;8(5):e64465. doi: 10.1371/journal.pone.0064465. PubMed PMID: 23717618; PubMed Central PMCID: PMC3663743.

229. Xu G, Strong MJ, Lacey MR, Baribault C, Flemington EK, Taylor CM. RNA CoMPASS: a dual approach for pathogen and host transcriptome analysis of RNA-seq datasets. *PloS one*. 2014;9(2):e89445. doi: 10.1371/journal.pone.0089445. PubMed PMID: 24586784; PubMed Central PMCID: PMC3934900.

230. Fernandez-Cuesta L, Sun R, Menon R, George J, Lorenz S, Meza-Zepeda LA, et al. Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. *Genome biology*. 2015;16:7. doi: 10.1186/s13059-014-0558-0. PubMed PMID: 25650807; PubMed Central PMCID: PMC4300615.

231. Yorukoglu D, Hach F, Swanson L, Collins CC, Birol I, Sahinalp SC. Dissect: detection and characterization of novel structural alterations in transcribed sequences. *Bioinformatics*. 2012;28(12):i179-87. doi: 10.1093/bioinformatics/bts214. PubMed PMID: 22689759; PubMed Central PMCID: PMC3371846.

232. Torres-Garcia W, Zheng S, Sivachenko A, Vegesna R, Wang Q, Yao R, et al. PRADA: pipeline for RNA sequencing data analysis. *Bioinformatics*. 2014;30(15):2224-6. doi: 10.1093/bioinformatics/btu169. PubMed PMID: 24695405; PubMed Central PMCID: PMC4103589.

233. Abate F, Zairis S, Ficarra E, Acquaviva A, Wiggins CH, Frattini V, et al. Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. *BMC Syst Biol*. 2014;8(1):97. doi: 10.1186/s12918-014-0097-z. PubMed PMID: 25183062; PubMed Central PMCID: PMC4363948.

234. Iyer MK, Chinnaiyan AM, Maher CA. ChimeraScan: a tool for identifying chimeric transcription in sequencing data. *Bioinformatics*. 2011;27(20):2903-4. doi: 10.1093/bioinformatics/btr467. PubMed PMID: 21840877; PubMed Central PMCID: PMC3187648.

235. Kim D, Salzberg SL. TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. *Genome biology*. 2011;12(8):R72. doi: 10.1186/gb-2011-12-8-r72. PubMed PMID: 21835007; PubMed Central PMCID: PMC3245612.

236. Chen K, Wallis JW, Kandoth C, Kalicki-Veizer JM, Mungall KL, Mungall AJ, et al. BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. *Bioinformatics*. 2012;28(14):1923-4. doi: 10.1093/bioinformatics/bts272. PubMed PMID: 22563071; PubMed Central PMCID: PMC3389765.

237. McPherson A, Hormozdiari F, Zayed A, Giuliany R, Ha G, Sun MG, et al. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. *PLoS computational biology*. 2011;7(5):e1001138. doi: 10.1371/journal.pcbi.1001138. PubMed PMID: 21625565; PubMed Central PMCID: PMC3098195.

238. Li Y, Chien J, Smith DI, Ma J. FusionHunter: identifying fusion transcripts in cancer using paired-end RNA-seq. *Bioinformatics*. 2011;27(12):1708-10. doi: 10.1093/bioinformatics/btr265. PubMed PMID: 21546395.

239. Benelli M, Pescucci C, Marseglia G, Severgnini M, Torricelli F, Magi A. Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. *Bioinformatics*. 2012;28(24):3232-9. doi: 10.1093/bioinformatics/bts617. PubMed PMID: 23093608.
240. Swanson L, Robertson G, Mungall KL, Butterfield YS, Chiu R, Corbett RD, et al. Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. *BMC genomics*. 2013;14:550. doi: 10.1186/1471-2164-14-550. PubMed PMID: 23941359; PubMed Central PMCID: PMC3751903.
241. Abate F, Acquaviva A, Paciello G, Foti C, Ficarra E, Ferrarini A, et al. Bellerophon: an RNA-Seq data analysis framework for chimeric transcripts discovery based on accurate fusion model. *Bioinformatics*. 2012;28(16):2114-21. doi: 10.1093/bioinformatics/bts334. PubMed PMID: 22711792.
242. Kalyana-Sundaram S, Shanmugam A, Chinnaiyan AM. Gene Fusion Markup Language: a prototype for exchanging gene fusion data. *BMC bioinformatics*. 2012;13:269. doi: 10.1186/1471-2105-13-269. PubMed PMID: 23072312; PubMed Central PMCID: PMC3607969.
243. Gulleage AA, Vora H, Patel K, Loraine AE. A protocol for visual analysis of alternative splicing in RNA-Seq data using integrated genome browser. *Methods in molecular biology*. 2014;1158:123-37. Epub 2014/05/06. doi: 10.1007/978-1-4939-0700-7_8. PubMed PMID: 24792048; PubMed Central PMCID: PMC4070736.
244. Loraine AE, Blakley IC, Jagadeesan S, Harper J, Miller G, Firon N. Analysis and Visualization of RNA-Seq Expression Data Using RStudio, Bioconductor, and Integrated Genome Browser. *Methods in molecular biology*. 2015;1284:481-501. Epub 2015/03/12. doi: 10.1007/978-1-4939-2444-8_24. PubMed PMID: 25757788; PubMed Central PMCID: PMC4387895.
245. Liu Q, Chen C, Shen E, Zhao F, Sun Z, Wu J. Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. *Genomics*. 2012;99(3):178-82. doi: 10.1016/j.ygeno.2011.12.003. PubMed PMID: 22226708.
246. Tokheim C, Park JW, Xing Y. PrimerSeq: Design and visualization of RT-PCR primers for alternative splicing using RNA-seq data. *Genomics, proteomics & bioinformatics*. 2014;12(2):105-9. doi: 10.1016/j.gpb.2014.04.001. PubMed PMID: 24747190.
247. Foissac S, Sammeth M. Analysis of alternative splicing events in custom gene datasets by AStalavista. *Methods in molecular biology*. 2015;1269:379-92. doi: 10.1007/978-1-4939-2291-8_24. PubMed PMID: 25577392.
248. Krzywinski M, Schein J, Birol I, Connors J, Gascoyne R, Horsman D, et al. Circos: an information aesthetic for comparative genomics. *Genome research*. 2009;19(9):1639-45. doi: 10.1101/gr.092759.109. PubMed PMID: 19541911; PubMed Central PMCID: PMC2752132.
249. Chelaru F, Smith L, Goldstein N, Bravo HC. Epiviz: interactive visual analytics for functional genomics data. *Nature methods*. 2014;11(9):938-40. doi: 10.1038/nmeth.3038. PubMed PMID: 25086505; PubMed Central PMCID: PMC4149593.
250. Mariette J, Noirot C, Nabihoudine I, Bardou P, Hoede C, Djari A, et al. RNAbrowse: RNA-Seq de novo assembly results browser. *PloS one*. 2014;9(5):e96821. doi: 10.1371/journal.pone.0096821. PubMed PMID: 24823498; PubMed Central PMCID: PMC4019526.
251. Severin J, Lizio M, Harshbarger J, Kawaji H, Daub CO, Hayashizaki Y, et al. Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. *Nature biotechnology*. 2014;32(3):217-9. doi: 10.1038/nbt.2840. PubMed PMID: 24727769.
252. Roge X, Zhang X. RNAseqViewer: visualization tool for RNA-Seq data. *Bioinformatics*. 2014;30(6):891-2. doi: 10.1093/bioinformatics/btt649. PubMed PMID: 24215023.

253. Watson M, Schnettler E, Kohl A. viRome: an R package for the visualization and analysis of viral small RNA sequence datasets. *Bioinformatics*. 2013;29(15):1902-3. doi: 10.1093/bioinformatics/btt297. PubMed PMID: 23709497; PubMed Central PMCID: PMC3712215.
254. Jang I, Chang H, Jun Y, Park S, Yang JO, Lee B, et al. miRseqViewer: multi-panel visualization of sequence, structure and expression for analysis of microRNA sequencing data. *Bioinformatics*. 2015;31(4):596-8. doi: 10.1093/bioinformatics/btu676. PubMed PMID: 25322835.
255. Crabtree J, Agrawal S, Mahurkar A, Myers GS, Rasko DA, White O. Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. *Bioinformatics*. 2014;30(21):3125-7. doi: 10.1093/bioinformatics/btu505. PubMed PMID: 25075113; PubMed Central PMCID: PMC4201160.
256. An J, Lai J, Wood DL, Sajjanhar A, Wang C, Tevz G, et al. RNASeqBrowser: A genome browser for simultaneous visualization of raw strand specific RNAseq reads and UCSC genome browser custom tracks. *BMC genomics*. 2015;16:145. doi: 10.1186/s12864-015-1346-2. PubMed PMID: 25766521; PubMed Central PMCID: PMC4355470.
257. Shirley BC, Mucaki EJ, Whitehead T, Costea PI, Akan P, Rogan PK. Interpretation, stratification and evidence for sequence variants affecting mRNA splicing in complete human genome sequences. *Genomics, proteomics & bioinformatics*. 2013;11(2):77-85. Epub 2013/03/19. doi: 10.1016/j.gpb.2013.01.008. PubMed PMID: 23499923.
258. Viner C, Dorman SN, Shirley BC, Rogan PK. Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. *F1000Res*. 2014;3:8. doi: 10.12688/f1000research.3-8.v2. PubMed PMID: 24741438; PubMed Central PMCID: PMC3983938.
259. Spinelli R, Pirola A, Redaelli S, Sharma N, Raman H, Valletta S, et al. Identification of novel point mutations in splicing sites integrating whole-exome and RNA-seq data in myeloproliferative diseases. *Mol Genet Genomic Med*. 2013;1(4):246-59. doi: 10.1002/mgg3.23. PubMed PMID: 24498620; PubMed Central PMCID: PMC3865592.
260. McPherson A, Wu C, Wyatt AW, Shah S, Collins C, Sahinalp SC. nFuse: discovery of complex genomic rearrangements in cancer using high-throughput sequencing. *Genome research*. 2012;22(11):2250-61. doi: 10.1101/gr.136572.111. PubMed PMID: 22745232; PubMed Central PMCID: PMC3483554.
261. Chen EA, Souaiaia T, Herstein JS, Evgrafov OV, Spitsyna VN, Rebolini DF, et al. Effect of RNA integrity on uniquely mapped reads in RNA-Seq. *BMC research notes*. 2014;7:753. Epub 2014/10/24. doi: 10.1186/1756-0500-7-753. PubMed PMID: 25339126; PubMed Central PMCID: PMC4213542.
262. Gallego Romero I, Pai AA, Tung J, Gilad Y. RNA-seq: impact of RNA degradation on transcript quantification. *BMC biology*. 2014;12:42. Epub 2014/06/03. doi: 10.1186/1741-7007-12-42. PubMed PMID: 24885439; PubMed Central PMCID: PMC4071332.
263. Kumar R, Ichihashi Y, Kimura S, Chitwood DH, Headland LR, Peng J, et al. A High-Throughput Method for Illumina RNA-Seq Library Preparation. *Frontiers in plant science*. 2012;3:202. Epub 2012/09/14. doi: 10.3389/fpls.2012.00202. PubMed PMID: 22973283; PubMed Central PMCID: PMC3428589.
264. Bhargava V, Head SR, Ordoukhanian P, Mercola M, Subramaniam S. Technical variations in low-input RNA-seq methodologies. *Scientific reports*. 2014;4:3678. Epub 2014/01/15. doi: 10.1038/srep03678. PubMed PMID: 24419370; PubMed Central PMCID: PMC3890974.
265. Christodoulou DC, Gorham JM, Herman DS, Seidman JG. Construction of normalized RNA-seq libraries for next-generation sequencing using the crab duplex-specific nuclease.

Current protocols in molecular biology / edited by Frederick M Ausubel [et al]. 2011;Chapter 4:Unit4 12. Epub 2011/04/08. doi: 10.1002/0471142727.mb0412s94. PubMed PMID: 21472699; PubMed Central PMCID: PMC3152986.

266. Cabanski CR, Magrini V, Griffith M, Griffith OL, McGrath S, Zhang J, et al. cDNA hybrid capture improves transcriptome analysis on low-input and archived samples. *The Journal of molecular diagnostics : JMD*. 2014;16(4):440-51. Epub 2014/05/13. doi: 10.1016/j.jmoldx.2014.03.004. PubMed PMID: 24814956; PubMed Central PMCID: PMC4078367.

267. Norton N, Sun Z, Asmann YW, Serie DJ, Necela BM, Bhagwate A, et al. Gene expression, single nucleotide variant and fusion transcript discovery in archival material from breast tumors. *PloS one*. 2013;8(11):e81925. Epub 2013/11/28. doi: 10.1371/journal.pone.0081925. PubMed PMID: 24278466; PubMed Central PMCID: PMC3838386.

268. Ma Y, Ambannavar R, Stephans J, Jeong J, Dei Rossi A, Liu ML, et al. Fusion transcript discovery in formalin-fixed paraffin-embedded human breast cancer tissues reveals a link to tumor progression. *PloS one*. 2014;9(4):e94202. Epub 2014/04/15. doi: 10.1371/journal.pone.0094202. PubMed PMID: 24727804; PubMed Central PMCID: PMC3984112.

269. Busby MA, Stewart C, Miller CA, Grzeda KR, Marth GT. Scotty: a web tool for designing RNA-Seq experiments to measure differential gene expression. *Bioinformatics*. 2013;29(5):656-7. Epub 2013/01/15. doi: 10.1093/bioinformatics/btt015. PubMed PMID: 23314327; PubMed Central PMCID: PMC3582267.

270. Fu GK, Xu W, Wilhelmy J, Mindrinos MN, Davis RW, Xiao W, et al. Molecular indexing enables quantitative targeted RNA sequencing and reveals poor efficiencies in standard library preparations. *Proceedings of the National Academy of Sciences of the United States of America*. 2014;111(5):1891-6. Epub 2014/01/23. doi: 10.1073/pnas.1323732111. PubMed PMID: 24449890; PubMed Central PMCID: PMC3918775.

271. Jiang L, Schlesinger F, Davis CA, Zhang Y, Li R, Salit M, et al. Synthetic spike-in standards for RNA-seq experiments. *Genome research*. 2011;21(9):1543-51. Epub 2011/08/06. doi: 10.1101/gr.121095.111. PubMed PMID: 21816910; PubMed Central PMCID: PMC3166838.

272. Katayama S, Tohonon V, Linnarsson S, Kere J. SAMstr: statistical test for differential expression in single-cell transcriptome with spike-in normalization. *Bioinformatics*. 2013;29(22):2943-5. Epub 2013/09/03. doi: 10.1093/bioinformatics/btt511. PubMed PMID: 23995393; PubMed Central PMCID: PMC3810855.

273. Mardis ER. Next-generation DNA sequencing methods. *Annual review of genomics and human genetics*. 2008;9:387-402. Epub 2008/06/26. doi: 10.1146/annurev.genom.9.081307.164359. PubMed PMID: 18576944.

274. Mardis ER. Next-generation sequencing platforms. *Annual review of analytical chemistry*. 2013;6:287-303. Epub 2013/04/09. doi: 10.1146/annurev-anchem-062012-092628. PubMed PMID: 23560931.

275. Grada A, Weinbrecht K. Next-generation sequencing: methodology and application. *The Journal of investigative dermatology*. 2013;133(8):e11. Epub 2013/07/17. doi: 10.1038/jid.2013.248. PubMed PMID: 23856935.

276. van Dijk EL, Auger H, Jaszczyszyn Y, Thermes C. Ten years of next-generation sequencing technology. *Trends in genetics : TIG*. 2014;30(9):418-26. Epub 2014/08/12. doi: 10.1016/j.tig.2014.07.001. PubMed PMID: 25108476.

277. Liu Y, Zhou J, White KP. RNA-seq differential expression studies: more sequence or more replication? *Bioinformatics*. 2014;30(3):301-4. Epub 2013/12/10. doi:

10.1093/bioinformatics/btt688. PubMed PMID: 24319002; PubMed Central PMCID: PMC3904521.

278. Sims D, Sudbery I, Illott NE, Heger A, Ponting CP. Sequencing depth and coverage: key considerations in genomic analyses. *Nature reviews Genetics*. 2014;15(2):121-32. Epub 2014/01/18. doi: 10.1038/nrg3642. PubMed PMID: 24434847.

279. Roberts A, Trapnell C, Donaghey J, Rinn JL, Pachter L. Improving RNA-Seq expression estimates by correcting for fragment bias. *Genome biology*. 2011;12(3):R22. Epub 2011/03/18. doi: 10.1186/gb-2011-12-3-r22. PubMed PMID: 21410973; PubMed Central PMCID: PMC3129672.

280. Wu TD, Nacu S. Fast and SNP-tolerant detection of complex variants and splicing in short reads. *Bioinformatics*. 2010;26(7):873-81. Epub 2010/02/12. doi: 10.1093/bioinformatics/btq057. PubMed PMID: 20147302; PubMed Central PMCID: PMC2844994.

281. Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B. Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nature methods*. 2008;5(7):621-8. Epub 2008/06/03. doi: 10.1038/nmeth.1226. PubMed PMID: 18516045.

282. Li B, Ruotti V, Stewart RM, Thomson JA, Dewey CN. RNA-Seq gene expression estimation with read mapping uncertainty. *Bioinformatics*. 2010;26(4):493-500. Epub 2009/12/22. doi: 10.1093/bioinformatics/btp692. PubMed PMID: 20022975; PubMed Central PMCID: PMC2820677.

283. Sultan M, Amstislavskiy V, Risch T, Schuette M, Dokel S, Ralser M, et al. Influence of RNA extraction methods and library selection schemes on RNA-seq data. *BMC genomics*. 2014;15:675. Epub 2014/08/13. doi: 10.1186/1471-2164-15-675. PubMed PMID: 25113896; PubMed Central PMCID: PMC4148917.

284. Wan Q, Dingerdissen H, Fan Y, Gulzar N, Pan Y, Wu TJ, et al. BioXpress: an integrated RNA-seq-derived gene expression database for pan-cancer analysis. *Database : the journal of biological databases and curation*. 2015;2015. Epub 2015/03/31. doi: 10.1093/database/bav019. PubMed PMID: 25819073.

285. Keen JC, Moore HM. The Genotype-Tissue Expression (GTEx) Project: Linking Clinical Data with Molecular Analysis to Advance Personalized Medicine. *Journal of personalized medicine*. 2015;5(1):22-9. Epub 2015/03/27. doi: 10.3390/jpm5010022. PubMed PMID: 25809799.

286. Kvam VM, Liu P, Si Y. A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data. *American journal of botany*. 2012;99(2):248-56. Epub 2012/01/24. doi: 10.3732/ajb.1100340. PubMed PMID: 22268221.

287. Risso D, Ngai J, Speed TP, Dudoit S. Normalization of RNA-seq data using factor analysis of control genes or samples. *Nature biotechnology*. 2014;32(9):896-902. Epub 2014/08/26. doi: 10.1038/nbt.2931. PubMed PMID: 25150836; PubMed Central PMCID: PMC4404308.